

GCGGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50
GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100
ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTTGCT 150
ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200
TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250
TTCAAAAAC TCAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300
ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350
ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400
CAAAACTTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450
AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500
TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550
ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600
TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650
GACTAGTATT CAAGAACCCA CAGAAATTTC TCTATCTTCC AAGCCAAGAG 700
CACCAAGAAC TACTCCCTTT CTTCAAGTTGA ATGAAATAAG AAATGTAAAA 750
CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800
TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTTCATG 850
TCTACTGTGA TGTTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900
ATAGATGGAT CACAAAACCT CAATGAAACG TGGGAGAACT ACAAATATGG 950
TTTTGGGAGG CTTGATGGAG AATTTTGGTT GGGCCTAGAG AAGATATACT 1000
CCATAGTGAA GCAATCTAAT TATGTTTTAC GAATTGAGTT GGAAGACTGG 1050
AAAGACAACA AACATTATAT TGAATATTCT TTTTACTTGG GAAATCACGA 1100
AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150
CAATCCCGGA AAACAAAGAT TTGGTGTTTT CTACTTGGGA TCACAAAGCA 1200
AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250

FIG. 1A-1

TGATGAGTGT	GGAGAAAACA	ACCTAAATGG	TAAATATAAC	AAACCAAGAG	1300
CAAAATCTAA	GCCAGAGAGG	AGAAGAGGAT	TATCTTGGAA	GTCTCAAAAT	1350
GGAAGGTTAT	ACTCTATAAA	ATCAACCAAA	ATGTTGATCC	ATCCAACAGA	1400
TTCAGAAAGC	TTTGAATGAA	CTGAGGCAAT	TTAAAGGCAT	ATTTAACCAT	1450
TAACTCATTC	CAAGTTAATG	TGGTCTAATA	ATCTGGTATA	AATCCTTAAG	1500
AGAAAGCTTG	AGAAATAGAT	TTTTTTTATC	TTAAAGTCAC	TGTCTATTTA	1550
AGATTAAACA	TACAATCACA	TAACCTTAAA	GAATACCGTT	TACATTTCTC	1600
AATCAAAATT	CTTATAATAC	TATTTGTTTT	AAATTTTGTG	ATGTGGGAAT	1650
CAATTTTAGA	TGGTCACAAT	CTAGATTATA	ATCAATAGGT	GAACTTATTA	1700
AATAACTTTT	CTAAATAAAA	AATTTAGAGA	CTTTTATTTT	AAAAGGCATC	1750
ATATGAGCTA	ATATCACAAC	TTTCCCAGTT	TAAAAAACTA	GTACTCTTGT	1800
TAAAACTCTA	AACTTGACTA	AATACAGAGG	ACTGGTAATT	GTACAGTTCT	1850
TAAATGTTGT	AGTATTAATT	TCAAAACTAA	AAATCGTCAG	CACAGAGTAT	1900
GTGTAAAAAT	CTGTAATACA	AATTTTTAAA	CTGATGCTTC	ATTTTGCTAC	1950
AAAATAATTT	GGAGTAAATG	TTTGATATGA	TTTATTTATG	AAACCTAATG	2000
AAGCAGAATT	AAATACTGTA	TTAAAATAAG	TTCGCTGTCT	TT	2042

FIG. 1A-2

Met	Phe	Thr	Ile	Lys	Leu	Leu	Leu	Phe	Ile	Val	Pro	Leu	Val	Ile
1				5					10					15
Ser	Ser	Arg	Ile	Asp	Gln	Asp	Asn	Ser	Ser	Phe	Asp	Ser	Leu	Ser
				20					25					30
Pro	Glu	Pro	Lys	Ser	Arg	Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile
				35					40					45
Leu	Ala	Asn	Gly	Leu	Leu	Gln	Leu	Gly	His	Gly	Leu	Lys	Asp	Phe
				50					55					60
Val	His	Lys	Thr	Lys	Gly	Gln	Ile	Asn	Asp	Ile	Phe	Gln	Lys	Leu
				65					70					75
Asn	Ile	Phe	Asp	Gln	Ser	Phe	Tyr	Asp	Leu	Ser	Leu	Gln	Thr	Ser
				80					85					90
Glu	Ile	Lys	Glu	Glu	Glu	Lys	Glu	Leu	Arg	Arg	Thr	Thr	Tyr	Lys
				95					100					105
Leu	Gln	Val	Lys	Asn	Glu	Glu	Val	Lys	Asn	Met	Ser	Leu	Glu	Leu
				110					115					120
Asn	Ser	Lys	Leu	Glu	Ser	Leu	Leu	Glu	Glu	Lys	Ile	Leu	Leu	Gln
				125					130					135
Gln	Lys	Val	Lys	Tyr	Leu	Glu	Glu	Gln	Leu	Thr	Asn	Leu	Ile	Gln
				140					145					150
Asn	Gln	Pro	Glu	Thr	Pro	Glu	His	Pro	Glu	Val	Thr	Ser	Leu	Lys
				155					160					165
Thr	Phe	Val	Glu	Lys	Gln	Asp	Asn	Ser	Ile	Lys	Asp	Leu	Leu	Gln
				170					175					180
Thr	Val	Glu	Asp	Gln	Tyr	Lys	Gln	Leu	Asn	Gln	Gln	His	Ser	Gln
				185					190					195
Ile	Lys	Glu	Ile	Glu	Asn	Gln	Leu	Arg	Arg	Thr	Ser	Ile	Gln	Glu
				200					205					210
Pro	Thr	Glu	Ile	Ser	Leu	Ser	Ser	Lys	Pro	Arg	Ala	Pro	Arg	Thr
				215					220					225
Thr	Pro	Phe	Leu	Gln	Leu	Asn	Glu	Ile	Arg	Asn	Val	Lys	His	Asp
				230					235					240

FIG. 1B-1

Gly	Ile	Pro	Ala	Glu	Cys	Thr	Thr	Ile	Tyr	Asn	Arg	Gly	Glu	His
				245					250					255
Thr	Ser	Gly	Met	Tyr	Ala	Ile	Arg	Pro	Ser	Asn	Ser	Gln	Val	Phe
				260					265					270
His	Val	Tyr	Cys	Asp	Val	Ile	Ser	Gly	Ser	Pro	Trp	Thr	Leu	Ile
				275					280					285
Gln	His	Arg	Ile	Asp	Gly	Ser	Gln	Asn	Phe	Asn	Glu	Thr	Trp	Glu
				290					295					300
Asn	Tyr	Lys	Tyr	Gly	Phe	Gly	Arg	Leu	Asp	Gly	Glu	Phe	Trp	Leu
				305					310					315
Gly	Leu	Glu	Lys	Ile	Tyr	Ser	Ile	Val	Lys	Gln	Ser	Asn	Tyr	Val
				320					325					330
Leu	Arg	Ile	Glu	Leu	Glu	Asp	Trp	Lys	Asp	Asn	Lys	His	Tyr	Ile
				335					340					345
Glu	Tyr	Ser	Phe	Tyr	Leu	Gly	Asn	His	Glu	Thr	Asn	Tyr	Thr	Leu
				350					355					360
His	Leu	Val	Ala	Ile	Thr	Gly	Asn	Val	Pro	Asn	Ala	Ile	Pro	Glu
				365					370					375
Asn	Lys	Asp	Leu	Val	Phe	Ser	Thr	Trp	Asp	His	Lys	Ala	Lys	Gly
				380					385					390
His	Phe	Asn	Cys	Pro	Glu	Gly	Tyr	Ser	Gly	Gly	Trp	Trp	Trp	His
				395					400					405
Asp	Glu	Cys	Gly	Glu	Asn	Asn	Leu	Asn	Gly	Lys	Tyr	Asn	Lys	Pro
				410					415					420
Arg	Ala	Lys	Ser	Lys	Pro	Glu	Arg	Arg	Arg	Gly	Leu	Ser	Trp	Lys
				425					430					435
Ser	Gln	Asn	Gly	Arg	Leu	Tyr	Ser	Ile	Lys	Ser	Thr	Lys	Met	Leu
				440					445					450
Ile	His	Pro	Thr	Asp	Ser	Glu	Ser	Phe	Glu					
				455					460					

FIG. 1B-2

GGCTGAGGGG	AGGCCCGGAG	CCTTTCTGGG	GCCTGGGGGA	TCCTCTTGCA	50
CTGGTGGGTG	GAGAGAAGCG	CCTGCAGCCA	ACCAGGGTCA	GGCTGTGCTC	100
ACAGTTTCCT	CTGGCGGCAT	GTAAAGGCTC	CACAAAGGAG	TTGGGAGTTC	150
AAATGAGGCT	GCTGCGGACG	GCCTGAGGAT	GGACCCCAAG	CCCTGGACCT	200
GCCGAGCGTG	GCACTGAGGC	AGCGGCTGAC	GCTACTGTGA	GGGAAAGAAG	250
GTTGTGAGCA	GCCCCGCAGG	ACCCCTGGCC	AGCCCTGGCC	CCAGCCTCTG	300
CCGGAGCCCT	CTGTGGAGGC	AGAGCCAGTG	GAGCCCAGTG	AGGCAGGGCT	350
GCTTGGCAGC	CACCGGCCTG	CAACTCAGGA	ACCCCTCCAG	AGGCCATGGA	400
CAGGCTGCCC	CGCTGACGGC	CAGGGTGAAG	CATGTGAGGA	GCCGCCCCGG	450
AGCCAAGCAG	GAGGGAAGAG	GCTTTCATAG	ATTCTATTCA	CAAAGAATAA	500
CCACCATTTT	GCAAGGACCA	TGAGGCCACT	GTGCGTGACA	TGCTGGTGGC	550
TCGGACTGCT	GGCTGCCATG	GGAGCTGTTG	CAGGCCAGGA	GGACGGTTTT	600
GAGGGCACTG	AGGAGGGCTC	GCCAAGAGAG	TTCATTTACC	TAAACAGGTA	650
CAAGCGGGCG	GGCGAGTCCC	AGGACAAGTG	CACCTACACC	TTCATTGTGC	700
CCCAGCAGCG	GGTCACGGGT	GCCATCTGCG	TCAACTCCAA	GGAGCCTGAG	750
GTGCTTCTGG	AGAACCGAGT	GCATAAGCAG	GAGCTAGAGC	TGCTCAACAA	800
TGAGCTGCTC	AAGCAGAAGC	GGCAGATCGA	GACGCTGCAG	CAGCTGGTGG	850
AGGTGGACGG	CGGCATTGTG	AGCGAGGTGA	AGCTGCTGCG	CAAGGAGAGC	900
CGCAACATGA	ACTCGCGGGT	CACGCAGCTC	TACATGCAGC	TCCTGCACGA	950
GATCATCCGC	AAGCGGGACA	ACGCGTTGGA	GCTCTCCCAG	CTGGAGAACA	1000
GGATCCTGAA	CCAGACAGCC	GACATGCTGC	AGCTGGCCAG	CAAGTACAAG	1050
GACCTGGAGC	ACAAGTACCA	GCACCTGGCC	ACACTGGCCC	ACAACCAATC	1100
AGAGATCATC	GCGCAGCTTG	AGGAGCACTG	CCAGAGGGTG	CCCTCGGCCA	1150
GGCCCGTCCC	CCAGCCACCC	CCCGCTGCCC	CGCCCCGGGT	CTACCAACCA	1200

FIG. 2A

CCCACCTACA	ACCGCATCAT	CAACCAGATC	TCTACCAACG	AGATCCAGAG	1250
TGACCAGAAC	CTGAAGGTGC	TGCCACCCCE	TCTGCCCACT	ATGCCCACTC	1300
TCACCAGCCT	CCCATCTTCC	ACCGACAAGC	CGTCGGGCCC	ATGGAGAGAC	1350
TGCCTGCAGG	CCCTGGAGGA	TGGCCACGAC	ACCAGCTCCA	TCTACCTGGT	1400
GAAGCCGGAG	AACACCAACC	GCCTCATGCA	GGTGTGGTGC	GACCAGAGAC	1450
ACGACCCCGG	GGGCTGGACC	GTCATCCAGA	GACGCCTGGA	TGGCTCTGTT	1500
AACTTCTTCA	GGAAGTGGGA	GACGTACAAG	CAAGGGTTTG	GGAACATTGA	1550
CGGCGAATAC	TGGCTGGGCC	TGGAGAACAT	TTACTGGCTG	ACGAACCAAG	1600
GCAACTACAA	ACTCCTGGTG	ACCATGGAGG	ACTGGTCCGG	CCGCAAAGTC	1650
TTTGCAGAAT	ACGCCAGTTT	CCGCCTGGAA	CCTGAGAGCG	AGTATTATAA	1700
GCTGCGGCTG	GGGCGCTACC	ATGGCAATGC	GGGTGACTCC	TTTACATGGC	1750
ACAACGGCAA	GCAGTTCACC	ACCCTGGACA	GAGATCATGA	TGTCTACACA	1800
GGAAACTGTG	CCCCTACTACCA	GAAGGGAGGC	TGGTGGTATA	ACGCCTGTGC	1850
CCACTCCAAC	CTCAACGGGG	TCTGGTACCG	CGGGGGCCAT	TACCGGAGCC	1900
GCTACCAGGA	CGGAGTCTAC	TGGGCTGAGT	TCCGAGGAGG	CTCTTACTCA	1950
CTCAAGAAAG	TGGTGATGAT	GATCCGACCG	AACCCCAACA	CCTTCCACTA	2000
AGCCAGCTCC	CCCTCCTGAC	CTCTCGTGGC	CATTGCCAGG	AGCCCACCCT	2050
GGTCACGCTG	GCCACAGCAC	AAAGAACAAC	TCCTCACCAG	TCATCCTGA	2100
GGCTGGGAGG	ACCGGGATGC	TGGATTCTGT	TTTCCGAAGT	CACTGCAGCG	2150
GATGATGGAA	CTGAATCGAT	ACGGTGTTTT	CTGTCCCTCC	TACTTTCCTT	2200
CACACCAGAC	AGCCCCTCAT	GTCTCCAGGA	CAGGACAGGA	CTACAGACAA	2250
CTCTTTCTTT	AAATAAATTA	AGTCTCTACA	ATAAAAAAAAA		2290

FIG. 2B

Met	Arg	Pro	Leu	Cys	Val	Thr	Cys	Trp	Trp	Leu	Gly	Leu	Leu	Ala	1	5	10	15
Ala	Met	Gly	Ala	Val	Ala	Gly	Gln	Glu	Asp	Gly	Phe	Glu	Gly	Thr	20	25	30	
Glu	Glu	Gly	Ser	Pro	Arg	Glu	Phe	Ile	Tyr	Leu	Asn	Arg	Tyr	Lys	35	40	45	
Arg	Ala	Gly	Glu	Ser	Gln	Asp	Lys	Cys	Thr	Tyr	Thr	Phe	Ile	Val	50	55	60	
Pro	Gln	Gln	Arg	Val	Thr	Gly	Ala	Ile	Cys	Val	Asn	Ser	Lys	Glu	65	70	75	
Pro	Glu	Val	Leu	Leu	Glu	Asn	Arg	Val	His	Lys	Gln	Glu	Leu	Glu	80	85	90	
Leu	Leu	Asn	Asn	Glu	Leu	Leu	Lys	Gln	Lys	Arg	Gln	Ile	Glu	Thr	95	100	105	
Leu	Gln	Gln	Leu	Val	Glu	Val	Asp	Gly	Gly	Ile	Val	Ser	Glu	Val	110	115	120	
Lys	Leu	Leu	Arg	Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr	125	130	135	
Gln	Leu	Tyr	Met	Gln	Leu	Leu	His	Glu	Ile	Ile	Arg	Lys	Arg	Asp	140	145	150	
Asn	Ala	Leu	Glu	Leu	Ser	Gln	Leu	Glu	Asn	Arg	Ile	Leu	Asn	Gln	155	160	165	
Thr	Ala	Asp	Met	Leu	Gln	Leu	Ala	Ser	Lys	Tyr	Lys	Asp	Leu	Glu	170	175	180	
His	Lys	Tyr	Gln	His	Leu	Ala	Thr	Leu	Ala	His	Asn	Gln	Ser	Glu	185	190	195	
Ile	Ile	Ala	Gln	Leu	Glu	Glu	His	Cys	Gln	Arg	Val	Pro	Ser	Ala	200	205	210	
Arg	Pro	Val	Pro	Gln	Pro	Pro	Pro	Ala	Ala	Pro	Pro	Arg	Val	Tyr	215	220	225	
Gln	Pro	Pro	Thr	Tyr	Asn	Arg	Ile	Ile	Asn	Gln	Ile	Ser	Thr	Asn	230	235	240	
Glu	Ile	Gln	Ser	Asp	Gln	Asn	Leu	Lys	Val	Leu	Pro	Pro	Pro	Leu	245	250	255	

FIG. 3A

Pro	Thr	Met	Pro	Thr	Leu	Thr	Ser	Leu	Pro	Ser	Ser	Thr	Asp	Lys	260	265	270
Pro	Ser	Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Glu	Asp	Gly	275	280	285
His	Asp	Thr	Ser	Ser	Ile	Tyr	Leu	Val	Lys	Pro	Glu	Asn	Thr	Asn	290	295	300
Arg	Leu	Met	Gln	Val	Trp	Cys	Asp	Gln	Arg	His	Asp	Pro	Gly	Gly	305	310	315
Trp	Thr	Val	Ile	Gln	Arg	Arg	Leu	Asp	Gly	Ser	Val	Asn	Phe	Phe	320	325	330
Arg	Asn	Trp	Glu	Thr	Tyr	Lys	Gln	Gly	Phe	Gly	Asn	Ile	Asp	Gly	335	340	345
Glu	Tyr	Trp	Leu	Gly	Leu	Glu	Asn	Ile	Tyr	Trp	Leu	Thr	Asn	Gln	350	355	360
Gly	Asn	Tyr	Lys	Leu	Leu	Val	Thr	Met	Glu	Asp	Trp	Ser	Gly	Arg	365	370	375
Lys	Val	Phe	Ala	Glu	Tyr	Ala	Ser	Phe	Arg	Leu	Glu	Pro	Glu	Ser	380	385	390
Glu	Tyr	Tyr	Lys	Leu	Arg	Leu	Gly	Arg	Tyr	His	Gly	Asn	Ala	Gly	395	400	405
Asp	Ser	Phe	Thr	Trp	His	Asn	Gly	Lys	Gln	Phe	Thr	Thr	Leu	Asp	410	415	420
Arg	Asp	His	Asp	Val	Tyr	Thr	Gly	Asn	Cys	Ala	His	Tyr	Gln	Lys	425	430	435
Gly	Gly	Trp	Trp	Tyr	Asn	Ala	Cys	Ala	His	Ser	Asn	Leu	Asn	Gly	440	445	450
Val	Trp	Tyr	Arg	Gly	Gly	His	Tyr	Arg	Ser	Arg	Tyr	Gln	Asp	Gly	455	460	465
Val	Tyr	Trp	Ala	Glu	Phe	Arg	Gly	Gly	Ser	Tyr	Ser	Leu	Lys	Lys	470	475	480
Val	Val	Met	Met	Ile	Arg	Pro	Asn	Pro	Asn	Thr	Phe	His			485	490	493

FIG. 3B

GCAGCTGGTT	ACTGCATTTTC	TCCATGTGGC	AGACAGAGCA	AAGCCACAAC	50
GCTTTCTCTG	CTGGATTAAA	GACGGCCCAC	AGACCAGAAC	TTCCACTATA	100
CTACTTAAAA	TTACATAGGT	GGCTTGTCAA	ATTCAATTGA	TTAGTATTGT	150
AAAAGGAAAA	AGAAGTTCCT	TCTTACAGCT	TGGATTCAAC	GGTCCAAAAC	200
AAAAATGCAG	CTGCCATTAA	AGTCTCAGAT	GAACAAACTT	CTACACTGAT	250
TTTTAAAATC	AAGAATAAGG	GCAGCAAGTT	TCTGGATTCA	CTGAATCAAC	300
AGACACAAAA	AGCTGGCAAT	ATAGCAACTA	TGAAGAGAAA	AGCTACTAAT	350
AAAATTAACC	CAACGCATAG	AAGACTTTTT	TTTCTCTTCT	AAAAACAAC	400
AAGTAAAGAC	TTAAATTTAA	ACACATCATT	TTACAACCTC	ATTTCAAAAT	450
GAAGACTTTT	ACCTGGACCC	TAGGTGTGCT	ATTCTTCCTA	CTAGTGGACA	500
CTGGACATTG	CAGAGGTGGA	CAATTCAAAA	TTAAAAAAT	AAACCAGAGA	550
AGATACCCTC	GTGCCACAGA	TGGTAAAGAG	GAAGCAAAGA	AATGTGCATA	600
CACATTCCTG	GTACCTGAAC	AAAGAATAAC	AGGGCCAATC	TGTGTCAACA	650
CCAAGGGGCA	AGATGCAAGT	ACCATTAAAG	ACATGATCAC	CAGGATGGAC	700
CTTGAAAACC	TGAAGGATGT	GCTCTCCAGG	CAGAAGCGGG	AGATAGATGT	750
TCTGCAACTG	GTGGTGGATG	TAGATGGAAA	CATTGTGAAT	GAGGTAAAGC	800
TGCTGAGAAA	GGAAAGCCGT	AACATGAACT	CTCGTGTTAC	TCAACTCTAT	850
ATGCAATTAT	TACATGAGAT	TATCCGTAAG	AGGGATAATT	CACTTGAAC	900
TTCCCAACTG	GAAAACAAAA	TCCTCAATGT	CACCACAGAA	ATGTTGAAGA	950
TGGCAACAAG	ATACAGGGAA	CTAGAGGTGA	AATACGCTTC	CTTGACTGAT	1000
CTTGTCAATA	ACCAATCTGT	GATGATCACT	TTGTTGGAAG	AACAGTGCTT	1050
GAGGATATTT	TCCCGACAAG	ACACCCATGT	GTCTCCCCCA	CTTGTCCAGG	1100
TGGTGCCACA	ACATATTCCT	AACAGCCAAC	AGTATACTCC	TGGTCTGCTG	1150
GGAGGTAACG	AGATTCAGAG	GGATCCAGGT	TATCCCAGAG	ATTTAATGCC	1200

FIG. 4A

ACCACCTGAT	CTGGCAACTT	CTCCCACCAA	AAGCCCTTTC	AAGATACCAC	1250
CGGTAAC TTT	CATCAATGAA	GGACCAT TCA	AAGACTGTCA	GCAAGCAAAA	1300
GAAGCTGGGC	ATTCGGTCAG	TGGGATTTAT	ATGATTAAAC	CTGAAAACAG	1350
CAATGGACCA	ATGCAGTTAT	GGTGTGAAAA	CAGTTTGGAC	CCTGGGGGTT	1400
GGACTGTTAT	TCAGAAAAGA	ACAGACGGCT	CTGTCAACTT	CTTCAGAAAT	1450
TGGGAAAATT	ATAAGAAAGG	GTTTGGAAAC	ATTGACGGAG	AATACTGGCT	1500
TGGACTGGAA	AATATCTATA	TGCTTAGCAA	TCAAGATAAT	TACAAGTTAT	1550
TGATTGAATT	AGAAGACTGG	AGTGATAAAA	AAGTCTATGC	AGAATACAGC	1600
AGCTTTCGTC	TGGAACCTGA	AAGTGAATTC	TATAGACTGC	GCCTGGGAAC	1650
TTACCAGGGA	AATGCAGGGG	ATTCTATGAT	GTGGCATAAT	GGTAAACAAT	1700
TCACCACACT	GGACAGAGAT	AAAGATATGT	ATGCAGGAAA	CTGCGCCCAC	1750
TTTCATAAAG	GAGGCTGGTG	GTACAATGCC	TGTGCACATT	CTAACCTAAA	1800
TGGAGTATGG	TACAGAGGAG	GCCATTACAG	AAGCAAGCAC	CAAGATGGAA	1850
TTTTCTGGGC	CGAATACAGA	GGCGGGTCAT	ACTCCTTAAG	AGCAGTTCAG	1900
ATGATGATCA	AGCCTATTGA	CTGAAGAGAG	ACACTCGCCA	ATTTAAATGA	1950
CACAGAACTT	TGTACTTTTC	AGCTCTTAAA	AATGTAAATG	TTACATGTAT	2000
ATTACTTGGC	ACAATTTATT	TCTACACAGA	AAGTTTTTAA	AATGAATTTT	2050
ACCGTAACTA	TAAAAGGGAA	CCTATAAATG	TAGTTTCATC	TGTCGTCAAT	2100
TACTGCAGAA	AATTATGTGT	ATCCACAACC	TAGTTATTTT	AAAAATTATG	2150
TTGACTAAAT	ACAAAGTTTG	TTTTCTAAAA	TGTAAATATT	TGCCACAATG	2200
TAAAGCAAAT	CTTAGCTATA	TTTTAAATCA	TAAATAACAT	GTTCAAGATA	2250
CTTAACAATT	TATTTAAAAT	CTAAGATTGC	TCTAACGTCT	AGTGAAAAAA	2300
ATATTTTTTA	AATTTTCAGCC	AAATAATGCA	TTTTATTTTA	TAAAAATACA	2350
GACAGAAAAT	TAGGGAGAAA	CTTCTAGTTT	TGCCAATAGA	AAATGTTCTT	2400

FIG. 4B

CCATTGAATA AAAGTTATTT CAAATTGAAT TTGTGCCTTT CACACGTAAT 2450
 GATTAAATCT GAATTCTTAA TAATATATCC TATGCTGATT TTCCCAAAC 2500
 ATGACCCATA GTATTAAATA CATATCATTT TAAAAATAA AAAAAAACCC 2550
 AAAAATAATG CATGCATAAT TTAAATGGTC AATTTATAAA GACAAATCTA 2600
 TGAATGAATT TTTCAGTGTT ATCTTCATAT GATATGCTGA ACACCAAAT 2650
 CTCCAGAAAT GCATTTTATG TAGTTCTAAA ATCAGCAAAA TATTGGTATT 2700
 AAAAAATGC AGAATATTTA GTGTGCTACA GATCTGAATT ATAGTTCTAA 2750
 TTTATTATTA CTTTTTTTCT AATTACTGA TCTTACTACT ACAAAGAAAA 2800
 AAAAACCCAA CCCATCTGCA ATTCAAATCA GAAAGTTTGG ACAGCTTTAC 2850
 AAGTATTAGT GCATGCTCAG AACAGGTGGG ACTAAAACAA ACTCAAGGAA 2900
 CTGTTGGCTG TTTTCCCGAT ACTGAGAATT CAACAGCTCC AGAGCAGAAG 2950
 CCACAGGGGC ATAGCTTAGT CCAAACCTGCT AATTTCATTT TACAGTGTAT 3000
 GTAACGCTTA GTCTCACAGT GTCTTTAACT CATCTTTGCA ATCAACAAC 3050
 TTACTAGTGA CTTTCTGGAA CAATTCCTT TCAGGAATAC ATATTCACTG 3100
 CTTAGAGGTG ACCTTGCCTT AATATATTTG TGAAGTTAAA ATTTTAAAGA 3150
 TAGCTCATGA AACTTTTGCT TAAGCAAAAA GAAACCTCG AATTGAAATG 3200
 TGTGAGGCAA ACTATGCATG GGAATAGCTT AATGTGAAGA TAATCATTTG 3250
 GACAACTCAA ATCCATCAAC ATGACCAATG TTTTTCATCT GCCACATCTC 3300
 AAAATAAAAC TTCTGGTGAA ACAAATTAAA CAAATATCC AAACCTCAAA 3350
 AAAAA 3355

FIG. 4C

Met	Lys	Thr	Phe	Thr	Trp	Thr	Leu	Gly	Val	Leu	Phe	Phe	Leu	Leu	1	5	10	15
Val	Asp	Thr	Gly	His	Cys	Arg	Gly	Gly	Gln	Phe	Lys	Ile	Lys	Lys	20	25	30	
Ile	Asn	Gln	Arg	Arg	Tyr	Pro	Arg	Ala	Thr	Asp	Gly	Lys	Glu	Glu	35	40	45	
Ala	Lys	Lys	Cys	Ala	Tyr	Thr	Phe	Leu	Val	Pro	Glu	Gln	Arg	Ile	50	55	60	
Thr	Gly	Pro	Ile	Cys	Val	Asn	Thr	Lys	Gly	Gln	Asp	Ala	Ser	Thr	65	70	75	
Ile	Lys	Asp	Met	Ile	Thr	Arg	Met	Asp	Leu	Glu	Asn	Leu	Lys	Asp	80	85	90	
Val	Leu	Ser	Arg	Gln	Lys	Arg	Glu	Ile	Asp	Val	Leu	Gln	Leu	Val	95	100	105	
Val	Asp	Val	Asp	Gly	Asn	Ile	Val	Asn	Glu	Val	Lys	Leu	Leu	Arg	110	115	120	
Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr	Gln	Leu	Tyr	Met	125	130	135	
Gln	Leu	Leu	His	Glu	Ile	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Leu	Glu	140	145	150	
Leu	Ser	Gln	Leu	Glu	Asn	Lys	Ile	Leu	Asn	Val	Thr	Thr	Glu	Met	155	160	165	
Leu	Lys	Met	Ala	Thr	Arg	Tyr	Arg	Glu	Leu	Glu	Val	Lys	Tyr	Ala	170	175	180	
Ser	Leu	Thr	Asp	Leu	Val	Asn	Asn	Gln	Ser	Val	Met	Ile	Thr	Leu	185	190	195	
Leu	Glu	Glu	Gln	Cys	Leu	Arg	Ile	Phe	Ser	Arg	Gln	Asp	Thr	His	200	205	210	
Val	Ser	Pro	Pro	Leu	Val	Gln	Val	Val	Pro	Gln	His	Ile	Pro	Asn	215	220	225	
Ser	Gln	Gln	Tyr	Thr	Pro	Gly	Leu	Leu	Gly	Gly	Asn	Glu	Ile	Gln	230	235	240	
Arg	Asp	Pro	Gly	Tyr	Pro	Arg	Asp	Leu	Met	Pro	Pro	Pro	Asp	Leu	245	250	255	

FIG. 5A

Ala	Thr	Ser	Pro	Thr	Lys	Ser	Pro	Phe	Lys	Ile	Pro	Pro	Val	Thr
				260					265					270
Phe	Ile	Asn	Glu	Gly	Pro	Phe	Lys	Asp	Cys	Gln	Gln	Ala	Lys	Glu
				275					280					285
Ala	Gly	His	Ser	Val	Ser	Gly	Ile	Tyr	Met	Ile	Lys	Pro	Glu	Asn
				290					295					300
Ser	Asn	Gly	Pro	Met	Gln	Leu	Trp	Cys	Glu	Asn	Ser	Leu	Asp	Pro
				305					310					315
Gly	Gly	Trp	Thr	Val	Ile	Gln	Lys	Arg	Thr	Asp	Gly	Ser	Val	Asn
				320					325					330
Phe	Phe	Arg	Asn	Trp	Glu	Asn	Tyr	Lys	Lys	Gly	Phe	Gly	Asn	Ile
				335					340					345
Asp	Gly	Glu	Tyr	Trp	Leu	Gly	Leu	Glu	Asn	Ile	Tyr	Met	Leu	Ser
				350					355					360
Asn	Gln	Asp	Asn	Tyr	Lys	Leu	Leu	Ile	Glu	Leu	Glu	Asp	Trp	Ser
				365					370					375
Asp	Lys	Lys	Val	Tyr	Ala	Glu	Tyr	Ser	Ser	Phe	Arg	Leu	Glu	Pro
				380					385					390
Glu	Ser	Glu	Phe	Tyr	Arg	Leu	Arg	Leu	Gly	Thr	Tyr	Gln	Gly	Asn
				395					400					405
Ala	Gly	Asp	Ser	Met	Met	Trp	His	Asn	Gly	Lys	Gln	Phe	Thr	Thr
				410					415					420
Leu	Asp	Arg	Asp	Lys	Asp	Met	Tyr	Ala	Gly	Asn	Cys	Ala	His	Phe
				425					430					435
His	Lys	Gly	Gly	Trp	Trp	Tyr	Asn	Ala	Cys	Ala	His	Ser	Asn	Leu
				440					445					450
Asn	Gly	Val	Trp	Tyr	Arg	Gly	Gly	His	Tyr	Arg	Ser	Lys	His	Gln
				455					460					465
Asp	Gly	Ile	Phe	Trp	Ala	Glu	Tyr	Arg	Gly	Gly	Ser	Tyr	Ser	Leu
				470					475					480
Arg	Ala	Val	Gln	Met	Met	Ile	Lys	Pro	Ile	Asp				
				485					490	491				

FIG. 5B

GGCTCAGAGG	CCCCACTGGA	CCCTCGGCTC	TTCCTTGGAC	TTCTTGTGTG	50
TTCTGTGAGC	TTCGCTGGAT	TCAGGGTCTT	GGGCATCAGA	GGTGAGAGGG	100
TGGGAAGGTC	CGCCGCGATG	GGGAAGCCCT	GGCTGCGTGC	GCTACAGCTG	150
CTGCTCCTGC	TGGGCGCGTC	GTGGGCGCGG	GCGGGCGCCC	CGCGCTGCAC	200
CTACACCTTC	GTGCTGCCCC	CGCAGAAGTT	CACGGGCGCT	GTGTGCTGGA	250
GCGGCCCCGC	ATCCACGCGG	GCGACGCCCC	AGGCCGCCAA	CGCCAGCGAG	300
CTGGCGGCGC	TGCGCATGCG	CGTCGGCCGC	CACGAGGAGC	TGTTACGCGA	350
GCTGCAGAGG	CTGGCGGCGG	CCGACGGCGC	CGTGGCCGGC	GAGGTGCGCG	400
CGCTGCGCAA	GGAGAGCCGC	GGCCTGAGCG	CGCGCCTGGG	CCAGTTGCGC	450
GCGCAGCTGC	AGCACGAGGC	GGGGCCCCGG	GCGGGCCCCG	GGGCGGATCT	500
GGGGGCGGAG	CCTGCCGCGG	CGCTGGCGCT	GCTCGGGGAG	CGCGTGCTCA	550
ACGCGTCCGC	CGAGGCTCAG	CGCGCAGCCG	CCCGGTCCA	CCAGCTGGAC	600
GTCAAGTTCC	GCGAGCTGGC	GCAGCTCGTC	ACCCAGCAGA	GCAGTCTCAT	650
CGCCCGCCTG	GAGCGCCTGT	GCCCCGGGAGG	CGCGGGCGGG	CAGCAGCAGG	700
TCCTGCCGCC	ACCCCCACTG	GTGCCTGTGG	TTCCGGTCCG	TCTTGTGGGT	750
AGCACCAGTG	ACACCAGTAG	GATGCTGGAC	CCAGCCCCAG	AGCCCCAGAG	800
AGACCAGACC	CAGAGACAGC	AGGAGCCCAT	GGCTTCTCCC	ATGCCTGCAG	850
GTCACCCTGC	GGTCCCCACC	AAGCCTGTGG	GCCCGTGGCA	GGATTGTGCA	900
GAGGCCCGCC	AGGCAGGCCA	TGAACAGAGT	GGAGTGTATG	AACTGCGAGT	950
GGGCCGTCAC	GTAGTGTCAG	TATGGTGTGA	GCAGCAACTG	GAGGGTGGAG	1000
GCTGGACTGT	GATCCAGCGG	AGGCAAGATG	G TTCAGTCAA	CTTCTTCACT	1050
ACCTGGCAGC	ACTATAAGGC	GGGCTTTGGG	CGGCCAGACG	GAGAATACTG	1100
GCTGGGCCTT	GAACCCGTGT	ATCAGCTGAC	CAGCCGTGGG	GACCATGAGC	1150
TGCTGGTTCT	CCTGGAGGAC	TGGGGGGGCC	GTGGAGCACG	TGCCCCACTAT	1200

FIG. 6A

GATGGCTTCT CCCTGGAACC CGAGAGCGAC CACTACCGCC TGC GGCTTGG 1250
CCAGTACCAT GGTGATGCTG GAGACTCTCT TTCCTGGCAC AATGACAAGC 1300
CCTTCAGCAC CGTGGATAGG GACCGAGACT CCTATTCTGG TAACTGTGCC 1350
CTGTACCAGC GGGGAGGCTG GTGGTACCAT GCCTGTGCCC ACTCCAACCT 1400
CAACGGTGTG TGGCACCACG GCGGCCACTA CCGAAGCCGC TACCAGGATG 1450
GTGTCTACTG GGCTGAGTTT CGTGGTGGGG CATATTCTCT CAGGAAGGCC 1500
GCCATGCTCA TTCGGCCCCT GAAGCTGTGA CTCTGTGTTC CTCTGTCCCC 1550
TAGGCCCTAG AGGACATTGG TCAGCAGGAG CCCAAGTTGT TCTGGCCACA 1600
CCTTCTTTGT GGCTCAGTGC CAATGTGTCC CACAGAACTT CCCACTGTGG 1650
ATCTGTGACC CTGGGCGCTG AAAATGGGAC CCAGGAATCC CCCCCGTCAA 1700
TATCTTGGCC TCAGATGGCT CCCCAAGGTC ATTCATATCT CGGTTTGAGC 1750
TCATATCTTA TAATAACACA AAGTAGCCAC 1780

FIG. 6B

Met	Gly	Lys	Pro	Trp	Leu	Arg	Ala	Leu	Gln	Leu	Leu	Leu	Leu	Leu	15
1				5					10						
Gly	Ala	Ser	Trp	Ala	Arg	Ala	Gly	Ala	Pro	Arg	Cys	Thr	Tyr	Thr	30
				20					25						
Phe	Val	Leu	Pro	Pro	Gln	Lys	Phe	Thr	Gly	Ala	Val	Cys	Trp	Ser	45
				35					40						
Gly	Pro	Ala	Ser	Thr	Arg	Ala	Thr	Pro	Glu	Ala	Ala	Asn	Ala	Ser	60
				50					55						
Glu	Leu	Ala	Ala	Leu	Arg	Met	Arg	Val	Gly	Arg	His	Glu	Glu	Leu	75
				65					70						
Leu	Arg	Glu	Leu	Gln	Arg	Leu	Ala	Ala	Ala	Asp	Gly	Ala	Val	Ala	90
				80					85						
Gly	Glu	Val	Arg	Ala	Leu	Arg	Lys	Glu	Ser	Arg	Gly	Leu	Ser	Ala	105
				95					100						
Arg	Leu	Gly	Gln	Leu	Arg	Ala	Gln	Leu	Gln	His	Glu	Ala	Gly	Pro	120
				110					115						
Gly	Ala	Gly	Pro	Gly	Ala	Asp	Leu	Gly	Ala	Glu	Pro	Ala	Ala	Ala	135
				125					130						
Leu	Ala	Leu	Leu	Gly	Glu	Arg	Val	Leu	Asn	Ala	Ser	Ala	Glu	Ala	150
				140					145						
Gln	Arg	Ala	Ala	Ala	Arg	Phe	His	Gln	Leu	Asp	Val	Lys	Phe	Arg	165
				155					160						
Glu	Leu	Ala	Gln	Leu	Val	Thr	Gln	Gln	Ser	Ser	Leu	Ile	Ala	Arg	180
				170					175						
Leu	Glu	Arg	Leu	Cys	Pro	Gly	Gly	Ala	Gly	Gly	Gln	Gln	Gln	Val	195
				185					190						
Leu	Pro	Pro	Pro	Pro	Leu	Val	Pro	Val	Val	Pro	Val	Arg	Leu	Val	210
				200					205						
Gly	Ser	Thr	Ser	Asp	Thr	Ser	Arg	Met	Leu	Asp	Pro	Ala	Pro	Glu	225
				215					220						
Pro	Gln	Arg	Asp	Gln	Thr	Gln	Arg	Gln	Gln	Glu	Pro	Met	Ala	Ser	240
				230					235						
Pro	Met	Pro	Ala	Gly	His	Pro	Ala	Val	Pro	Thr	Lys	Pro	Val	Gly	255
				245					250						

FIG. 7A

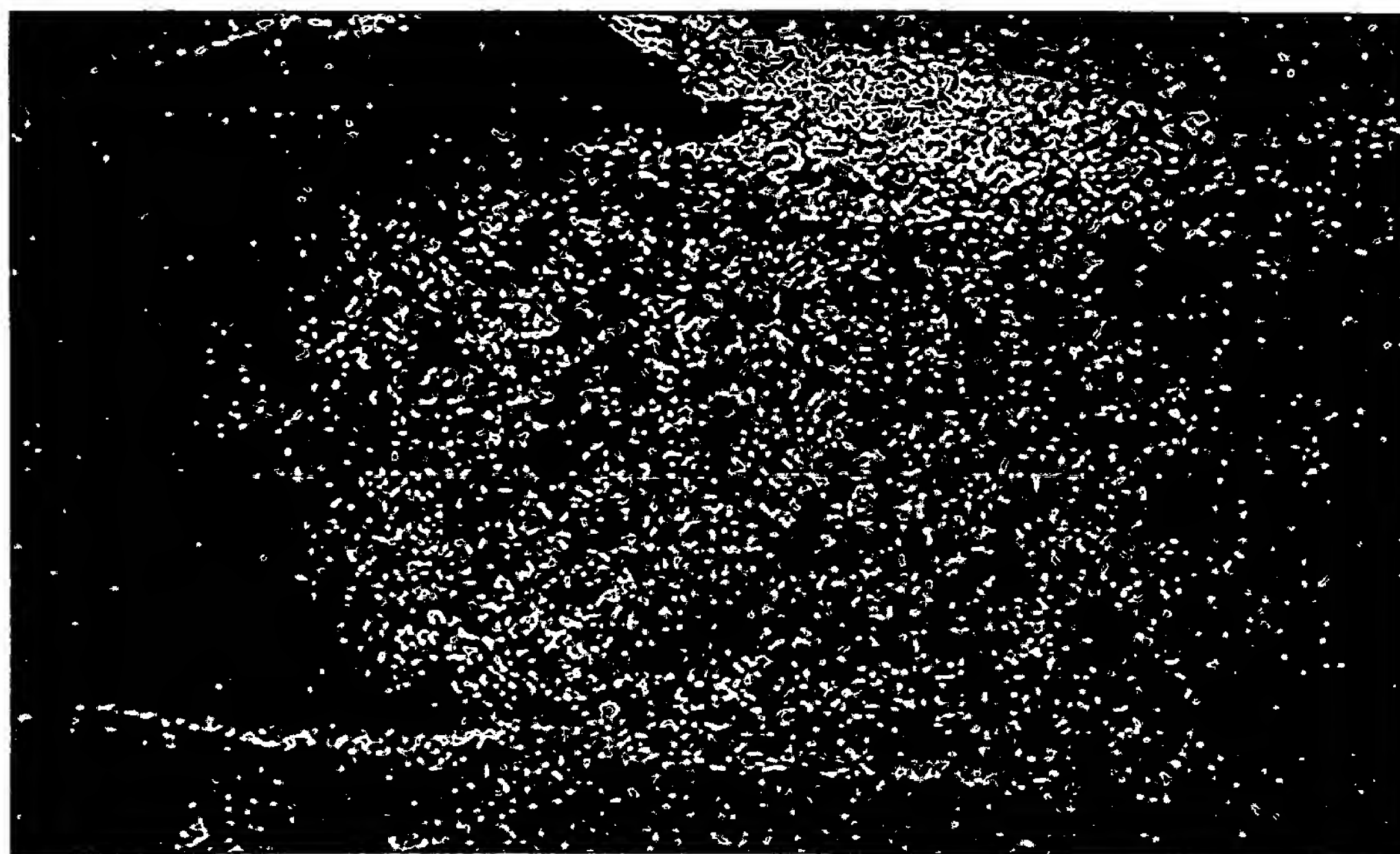
Pro	Trp	Gln	Asp	Cys	Ala	Glu	Ala	Arg	Gln	Ala	Gly	His	Glu	Gln	260	265	270
Ser	Gly	Val	Tyr	Glu	Leu	Arg	Val	Gly	Arg	His	Val	Val	Ser	Val	275	280	285
Trp	Cys	Glu	Gln	Gln	Leu	Glu	Gly	Gly	Gly	Trp	Thr	Val	Ile	Gln	290	295	300
Arg	Arg	Gln	Asp	Gly	Ser	Val	Asn	Phe	Phe	Thr	Thr	Trp	Gln	His	305	310	315
Tyr	Lys	Ala	Gly	Phe	Gly	Arg	Pro	Asp	Gly	Glu	Tyr	Trp	Leu	Gly	320	325	330
Leu	Glu	Pro	Val	Tyr	Gln	Leu	Thr	Ser	Arg	Gly	Asp	His	Glu	Leu	335	340	345
Leu	Val	Leu	Leu	Glu	Asp	Trp	Gly	Gly	Arg	Gly	Ala	Arg	Ala	His	350	355	360
Tyr	Asp	Gly	Phe	Ser	Leu	Glu	Pro	Glu	Ser	Asp	His	Tyr	Arg	Leu	365	370	375
Arg	Leu	Gly	Gln	Tyr	His	Gly	Asp	Ala	Gly	Asp	Ser	Leu	Ser	Trp	380	385	390
His	Asn	Asp	Lys	Pro	Phe	Ser	Thr	Val	Asp	Arg	Asp	Arg	Asp	Ser	395	400	405
Tyr	Ser	Gly	Asn	Cys	Ala	Leu	Tyr	Gln	Arg	Gly	Gly	Trp	Trp	Tyr	410	415	420
His	Ala	Cys	Ala	His	Ser	Asn	Leu	Asn	Gly	Val	Trp	His	His	Gly	425	430	435
Gly	His	Tyr	Arg	Ser	Arg	Tyr	Gln	Asp	Gly	Val	Tyr	Trp	Ala	Glu	440	445	450
Phe	Arg	Gly	Gly	Ala	Tyr	Ser	Leu	Arg	Lys	Ala	Ala	Met	Leu	Ile	455	460	465
Arg	Pro	Leu	Lys	Leu											470		

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FIG. 7B

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DNA 22779 DARK FIELD



THE WHITE SPOTS REPRESENT THE SILVER GRAINS.

FIG. 8A

DNA 22779 H&E

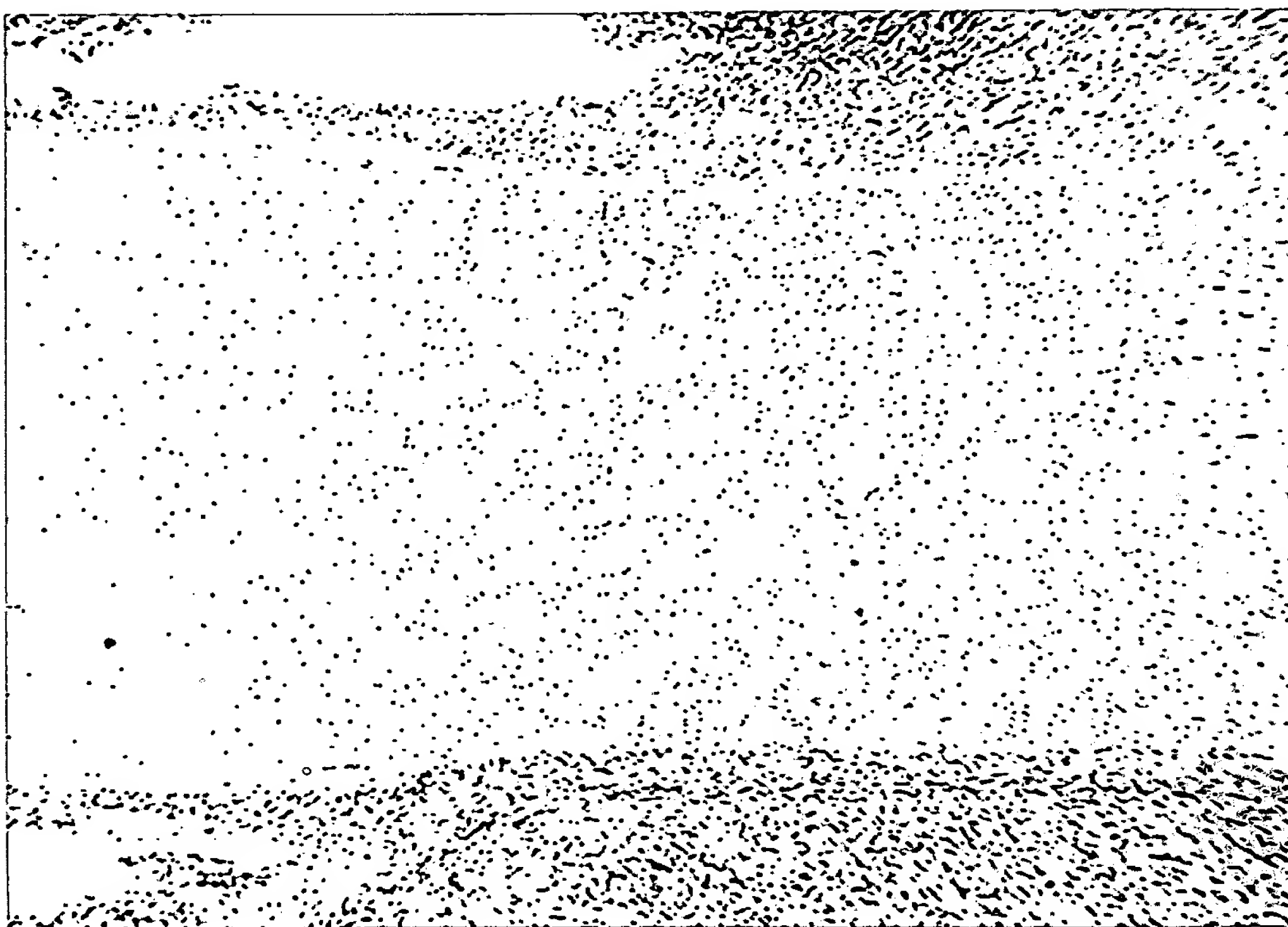


FIG. 8B

DNA 28497 H&E

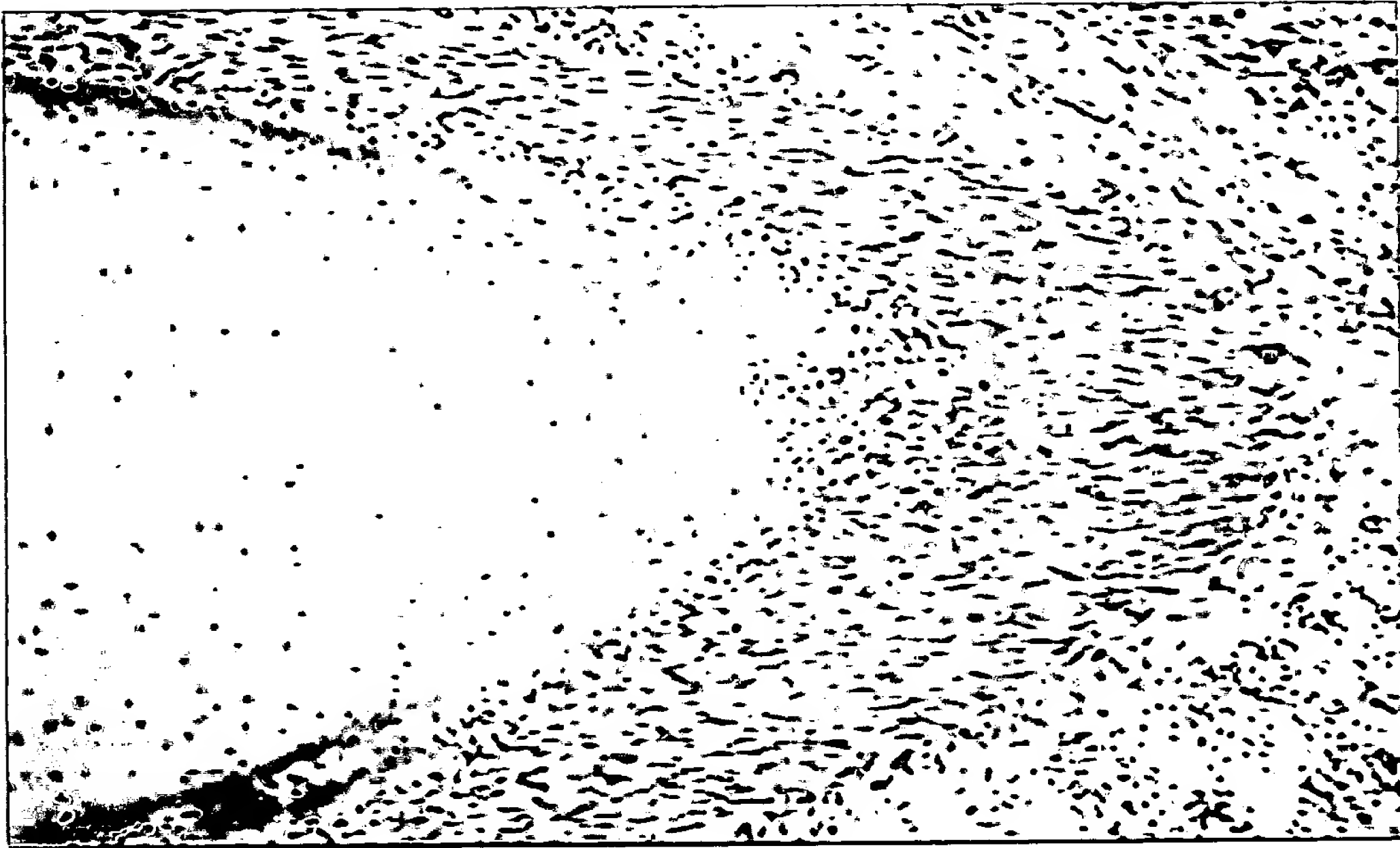
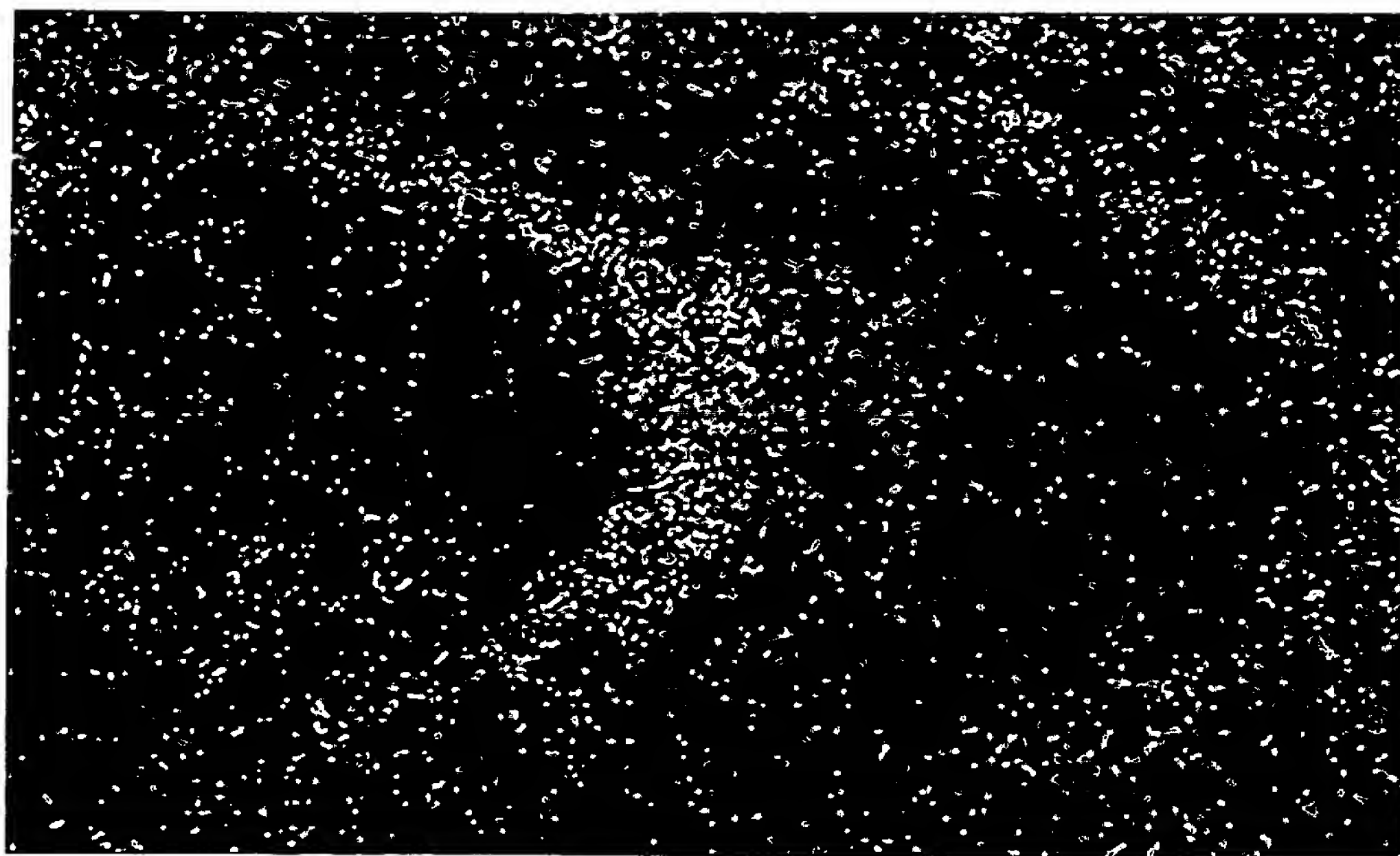


FIG. 9A

DNA 28497 DARK FIELD



THE WHITE SPOTS REPRESENT THE SILVER GRAINS.

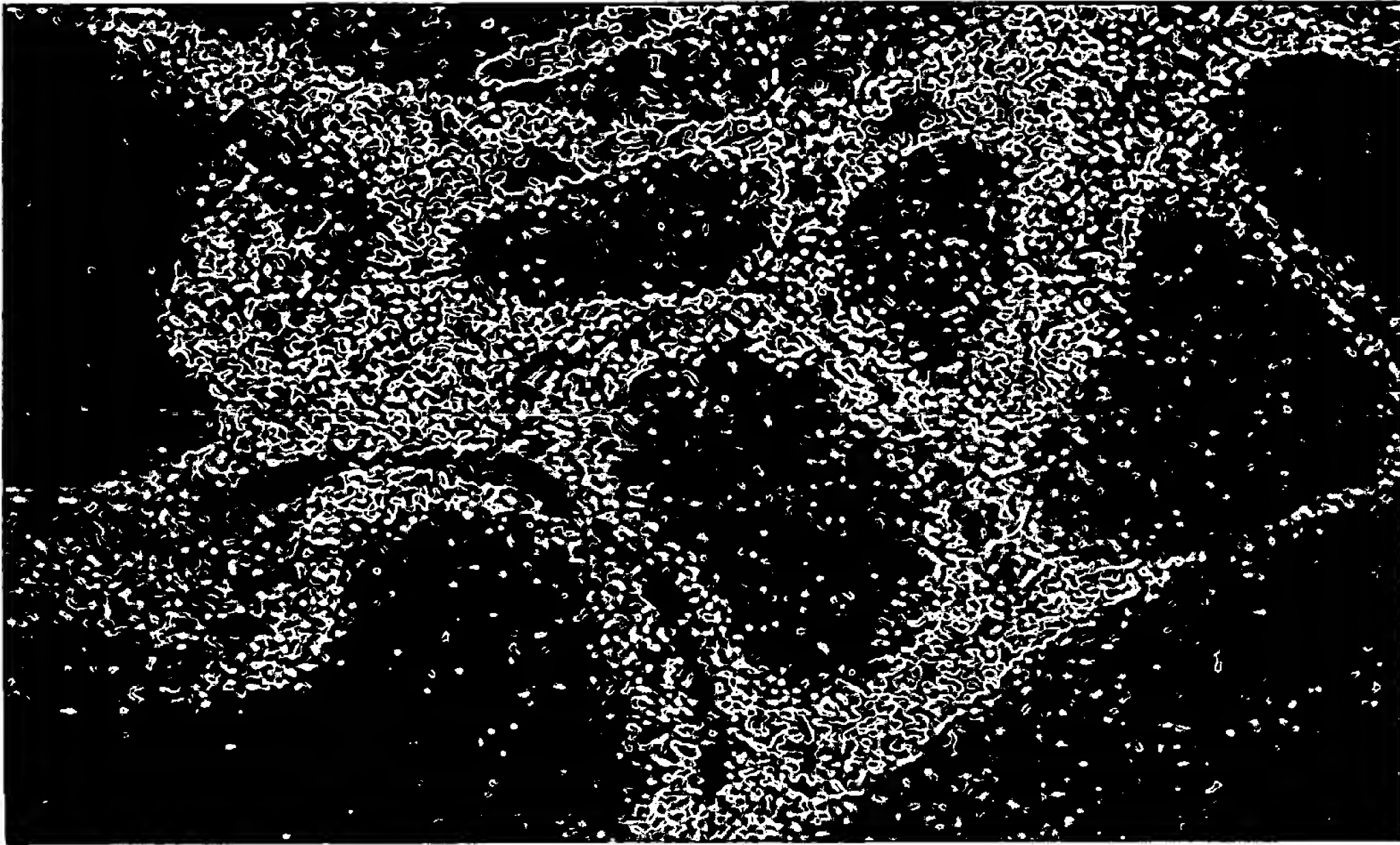
FIG. 9B

DNA 23339 H&E



FIG. 10A

DNA 23339 DARK FIELD



THE WHITE SPOTS REPRESENT THE SILVER GRAINS.

FIG. 10B

NL1 Northern

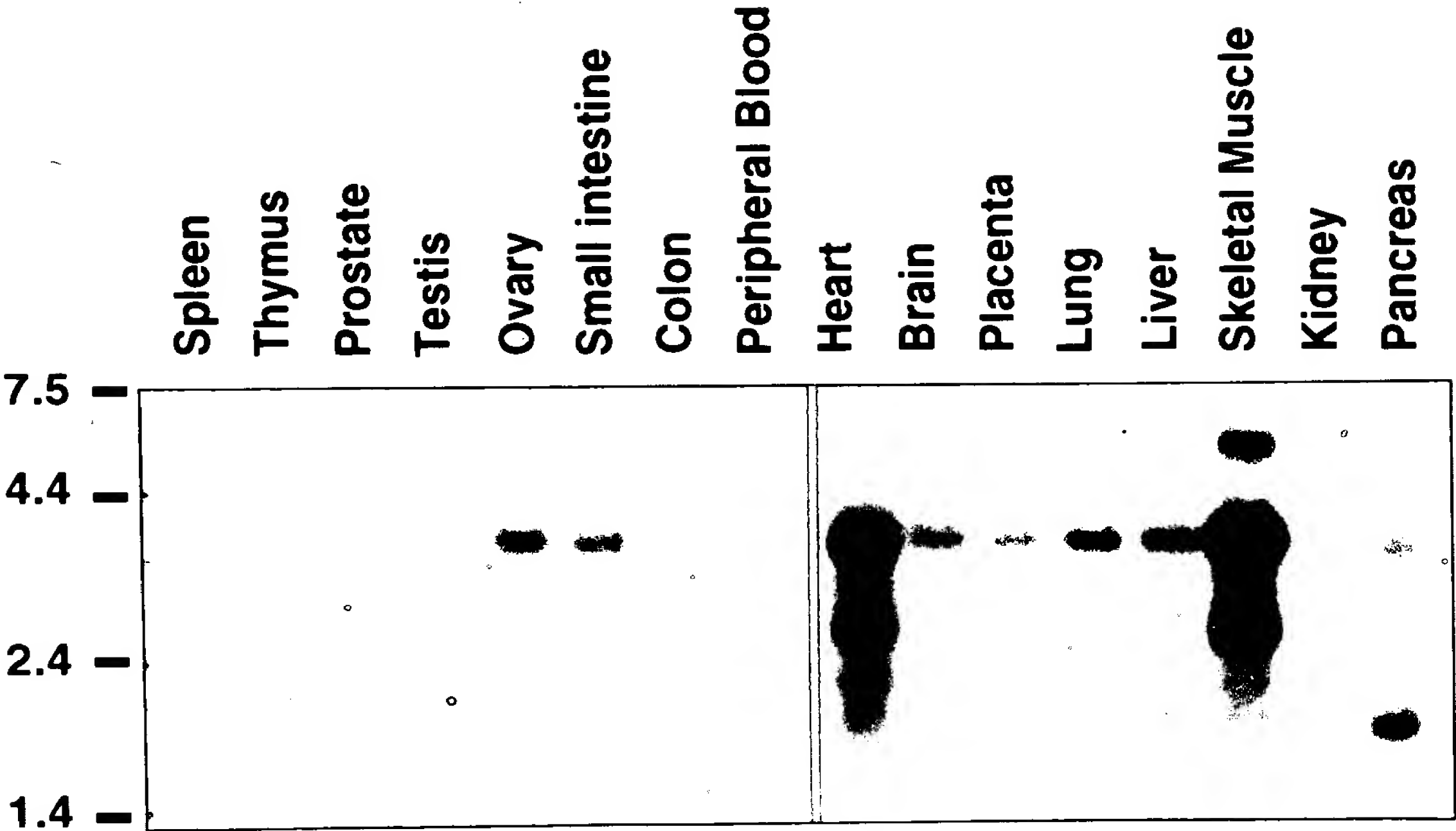


FIG. 11

NL5 Northern

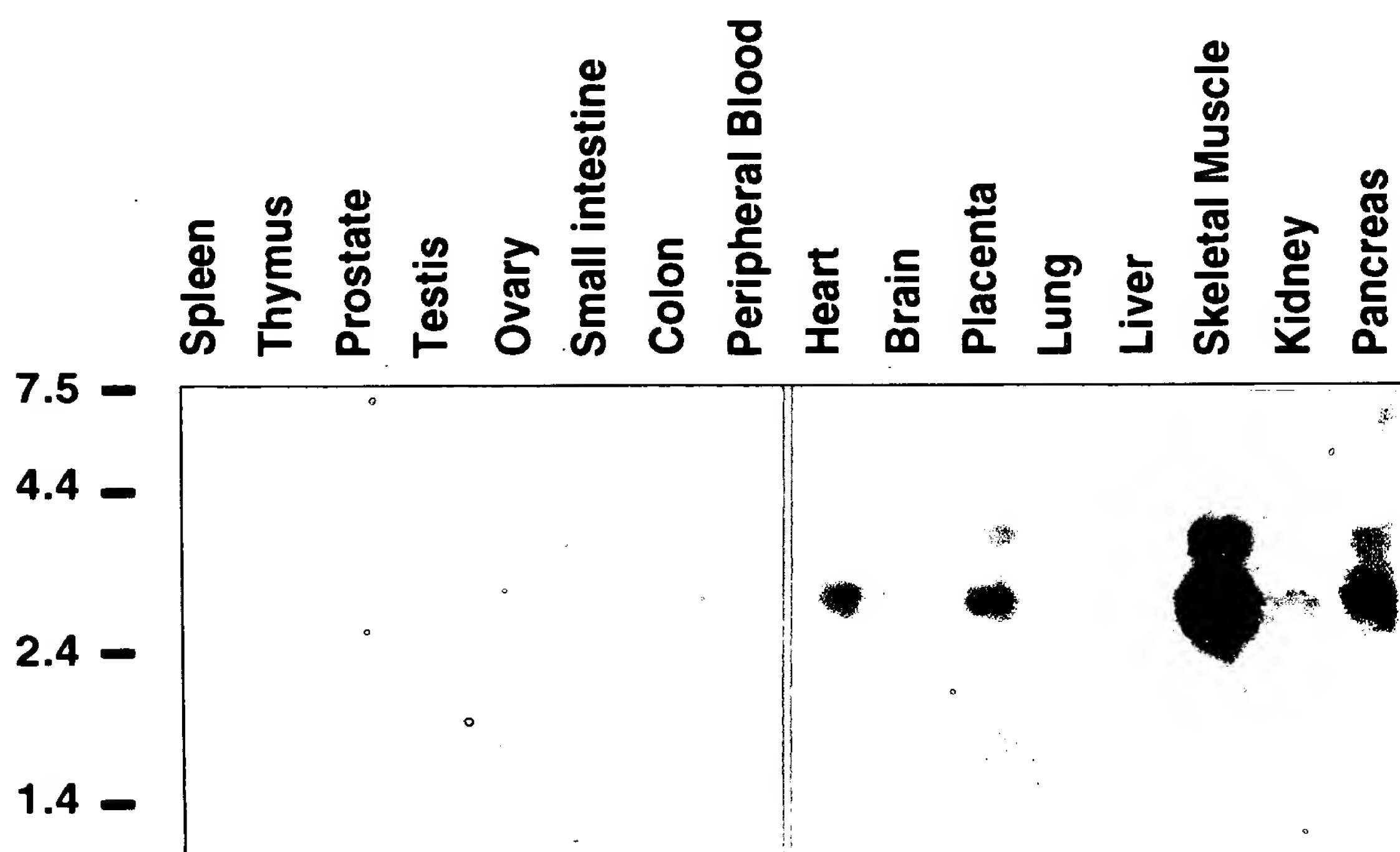


FIG. 12